AMENDMENTS TO THE SPECIFICATION:

On page 1, before line 1, please insert the following:

--Title of the Invention--

On page 1, before line 4, please insert the following:

--Cross Reference to Related Applications

This application is a national stage application of International Application PCT/EP2004/00709, filed June 30, 2004, designating the United States of America, which claims the benefit of Swedish Application No. 0301951-0, filed June 30, 2003, Provisional Application No. 60/481,043, filed June 30, 2003, and Provisional Application No. 60/481,319, filed September 1, 2003.--

On page 13, please replace the table and text extending from lines 3-16 with the following:

	CAGCAGCAGCAGCAGCAGCAGCAGCAG (SEQ ID NO:1)	Oligonucleotides which can be used in detection of CAG repeats
Variant 1	GTCG*TC* (SEQ ID NO:2) etc.	pGT, pCG, pTC
Variant 2	GTCG**TCGT***CGTC* (SEQ ID NO:3) etc.	PGTCC, pTCGT, pCGTC
Variant 3	GTCGT**CGTCG***TCGTC* (SEQ ID NO:4) etc.	PGTCGT, pCGTCG, pTCGTC
Variant 4	GTCGTCG**TCGTCGT***CGTCGTC* (SEQ ID NO:5) etc.	PGTCGTCG, pTCGTCGT, pCGTCGTC

Variant 1 describes three different types of di-mers (normal font, bold and italicized ~~underlined~~, respectively) of oligonucleotide to analyse two repeated units.

Variant 2 describes three different types of 4-mers (normal font, bold and italicized ~~underlined~~, respectively) of oligonucleotide to analyse 4 repeated units.

Variant 3 describes three different types of 5-mers (normal font, bold and italicized ~~underlined~~, respectively) of oligonucleotide to analyse 5 repeated units.

Variant 4 describes three different types of 7-mers (normal font, bold and italicized ~~underlined~~, respectively) of oligonucleotide to analyse 7 repeated units.

On page 14, please replace the table at lines 1-4 with the following:

	CGGCGGCGGCGGCGGCGGCGGCGGCGG (SEQ ID NO:6)	Oligonucleotides which can be used in detection of CGG repeats
Variant 1	GCCG*CC* (SEQ ID NO:7) etc.	pGC, pCG, pCC
Variant 2	GCCG**CCGC***CGCC* (SEQ ID NO:8) etc.	pGCCG, pCCGC, pCGCC
Variant 3	GCCGC**CGCCG***CCGCC* (SEQ ID NO:9) etc.	pGCCGC, pCGCCG, pCCGCC
Variant 4	GCCGCCG**CCGCCGC***CGCCGCC* (SEQ ID NO:10) etc.	pGCCGCCG, pCCGCCGC, pCGCCGCC

On page 33, please replace the paragraph extending between lines 6-9 with the following:

Example 1: Ligation of two oligonucleotides at a variable position in a gene with a thermocycled ligation reaction followed by bioluminescent detection

Oligonucleotides used

Name	5'-3'	Modification
BGL-1	ATGGTGCACCTGACTCCTGA (SEQ ID NO:11)	5' biotin
BGL-2	GGAGAAGTCTGCCGTTACTGC (SEQ ID NO:12)	5' P
BG-T	GCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCAT (SEQ ID NO:13)	

Complete upper strand

ATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGC (SEQ ID NO:14)

BG-S1 ACGGCAGACTTCTCC (SEQ ID NO:15)

On page 36, please replace the paragraph extending between lines 14-21 with the following:

Firstly a primer-template complex is formed by adding a oligonucleotide that is complementary to the sequence flanking the nucleotide repeat sequence under conditions ~~condtions~~ that allow annealing to occur:

Primer

Flanking sequence–CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG (SEQ ID NO:16) -flanking sequence

On page 36, please replace the paragraph extending between lines 26-31 with the following:

Add: pGCCG + ligase

Primer

Flanking sequence–CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG (SEQ ID NO:16) -flanking sequence

On page 37, please replace the paragraph extending between lines 11-15 with the following:

Add: pCCGC + ligase

PrimerGCCG

Flanking sequence–CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG (SEQ ID NO:16) -flanking sequence

On pages 37-38, please replace the paragraph extending between page 37, line 25 and page 38, line 14 with the following:

The experiment was based on the trinucleotide repeat (CAG/CTG) that is involved in a number of polyglutamine diseases (see table above). One picomole of oligonucleotide template with the sequence $(CTG)_{10}$ (SEQ ID NO:17) or $(CTG)_{20}$ (SEQ ID NO:18) was mixed with 40 picomoles of the complementary 5'-phosphorylated oligonucleotide, $(CAG)_3$ in 15 µl of Annealing Buffer (20 mM Tris-acetate, pH 7.6; 2 mM magnesium acetate) in a 96-well PSQ96 Plate. The short, phosphorylated oligonucleotide was annealed to the longer oligonucleotide templates by incubating for 5 minutes at 80°C and then allowed to cool to room temperature. Ligation was performed by adding 15 µl of Ligation Mix (200 U T4 DNA Ligase, 2 mM dATP, and 2 mM dithithreitol in Annealing Buffer) and incubating for 30 minutes at 37°C. Controls with Ligation Mix without ligase and $(CAG)_3$ (SEQ ID NO:19) were also run. Twenty-five microliters of the ligation reaction were treated with apyrase to digest excess dATP by adding 50 mU apyrase in 15 µl Annealing Buffer and incubating at room temperature (c. 25°C) for 25 minutes. To determine the amount of pyrophosphate produced by the ligation reaction, the PSQ96 Plate was transferred to a PSQ96 Pyrosequencing Instrument where 5 µl of Enzyme mix (25 mU sulphurylase and 0.5 µg luciferase in Annealing Buffer) and 5 µl of Substrate Mix (280 pmol APS and 7.5 µg luciferin in Annealing Buffer) were displaced by the instrument and the resulting light emission was detected. The signal obtained from known amounts of pyrophosphate and ATP was then determined by dispensing 5 picomoles of pyrophosphate into each well, followed by 5 picomoles of ATP. The results for triplicates, with signals from controls (without ligase and phosphorylated oligonucleotide), are shown in Fig. 6a.